



RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____

10/677,956B

Source: _____

TFW/6

Date Processed by STIC: _____

09/14/2006

ENTERED



IFW16

RAW SEQUENCE LISTING... DATE: 09/14/2006
PATENT APPLICATION: US/10/677,956B TIME: 15:32:14

Input Set : E:\16988.ST25.txt
Output Set: N:\CRF4\09142006\J677956B.raw

5 <110> APPLICANT: Zebedee, Suzanne
6 Inchauspe, Genevieve
7 Nasoff, Marc S.
8 Prince, Alfred M.
10 <120> TITLE OF INVENTION: METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT
VIRAL ANTIGENS
12 <130> FILE REFERENCE: 323-100USD
14 <140> CURRENT APPLICATION NUMBER: 10/677,956B
15 <141> CURRENT FILING DATE: 2003-10-01
17 <150> PRIOR APPLICATION NUMBER: 08/931,855
18 <151> PRIOR FILING DATE: 1997-09-16
20 <150> PRIOR APPLICATION NUMBER: 08/563,733
21 <151> PRIOR FILING DATE: 1995-11-08
23 <150> PRIOR APPLICATION NUMBER: 08/272,271
24 <151> PRIOR FILING DATE: 1994-07-08
26 <150> PRIOR APPLICATION NUMBER: 07/616,369
27 <151> PRIOR FILING DATE: 1990-11-21
29 <150> PRIOR APPLICATION NUMBER: 07/573,643
30 <151> PRIOR FILING DATE: 1990-08-27
32 <160> NUMBER OF SEQ ID NOS: 74
34 <170> SOFTWARE: PatentIn version 3.3
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 795
38 <212> TYPE: DNA
39 <213> ORGANISM: Human immunodeficiency virus
42 <220> FEATURE:
43 <221> NAME/KEY: CDS
44 <222> LOCATION: (16)..(789)
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49 1 5 10
51 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99
52 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
53 15 20 25
55 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147
56 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
57 30 35 40
59 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195
60 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
61 45 50 55 60
63 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243
64 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
65 65 70 75

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68 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
69                               80                               85                               90
71 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act      339
72 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
73                               95                               100                               105
75 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct      387
76 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
77                               110                               115                               120
79 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat      435
80 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
81 125                               130                               135                               140
83 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa      483
84 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
85                               145                               150                               155
87 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act      531
88 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
89                               160                               165                               170
91 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa      579
92 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
93                               175                               180                               185
95 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa      627
96 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
97                               190                               195                               200
99 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag      675
100 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
101 205                               210                               215                               220
103 gga gta gga gga ccc aaa aat caa caa tta tta tcc tta tgg ggg tgt      723
104 Gly Val Gly Gly Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys
105                               225                               230                               235
107 aaa ggg aaa ctt gtt tgt tat act tcc gtt aaa tgg aat gga ccc ggc      771
108 Lys Gly Lys Leu Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly
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117 <211> LENGTH: 258
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119 <213> ORGANISM: Human immunodeficiency virus
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128                               20                               25                               30
131 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
132                               35                               40                               45
135 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
136                               50                               55                               60

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139 Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
140 65 70 75 80
143 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
144 85 90 95
147 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
148 100 105 110
151 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
152 115 120 125
155 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
156 130 135 140
159 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
160 145 150 155 160
163 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
164 165 170 175
167 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
168 180 185 190
171 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
172 195 200 205
175 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
176 210 215 220
179 Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu
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184 245 250 255
187 Val Leu
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192 <211> LENGTH: 795
193 <212> TYPE: DNA
194 <213> ORGANISM: Human immunodeficiency virus
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (16)..(789)
201 <400> SEQUENCE: 3
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204 1 5 10
206 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99
207 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
208 15 20 25
210 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147
211 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
212 30 35 40
214 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195
215 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
216 45 50 55 60
218 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243
219 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
220 65 70 75
222 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att 291

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223 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
224      80      85      90
226 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act 339
227 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
228      95      100      105
230 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct 387
231 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
232      110      115      120
234 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat 435
235 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
236 125      130      135      140
238 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa 483
239 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
240      145      150      155
242 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act 531
243 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
244      160      165      170
246 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa 579
247 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu
248      175      180      185
250 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa 627
251 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys
252      190      195      200
254 gca ttg gga cca gcg gct aca cta gaa gaa atg atg aca gca tgt cag 675
255 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln
256 205      210      215      220
258 gga gta gga gga ccc aaa aat caa caa aga tta aat tta tgg ggg tgt 723
259 Gly Val Gly Gly Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys
260      225      230      235
262 aaa ggg aaa ctt att tgt tat act tcc gtt aaa tgg aat gga ccc ggc 771
263 Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly
264      240      245      250
266 cat aag gca aga gtt ttg taataa 795
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273 <212> TYPE: PRT
274 <213> ORGANISM: Human immunodeficiency virus
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283      20      25      30
286 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
287      35      40      45
290 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
291      50      55      60
294 Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu

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295 65              70              75              80
298 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
299              85              90              95
302 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
303              100              105              110
306 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
307              115              120              125
310 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
311              130              135              140
314 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
315 145              150              155              160
318 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
319              165              170              175
322 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
323              180              185              190
326 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
327              195              200              205
330 Ala Ala Thr Leu Glu Glu Met Thr Ala Cys Gln Gly Val Gly Gly
331              210              215              220
334 Pro Lys Asn Gln Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu
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338 Ile Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg
339              245              250              255
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348 <212> TYPE: DNA
349 <213> ORGANISM: Human immunodeficiency virus
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353 <221> NAME/KEY: CDS
354 <222> LOCATION: (16)..(789)
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359      1              5              10
361 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta      99
362 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
363      15              20              25
365 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta      147
366 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
367      30              35              40
369 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg      195
370 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
371 45              50              55              60
373 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag      243
374 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
375      65              70              75
377 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att      291
378 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile

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RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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Seq#:68,69,70,71,73,74

VERIFICATION SUMMARY

DATE: 09/14/2006

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Input Set : E:\16988.ST25.txt

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16988 ST25.txt

SEQUENCE LISTING

<110> Zebedee, Suzanne
Inchauspe, Genevieve
Nasoff, Marc S.
Prince, Alfred M.

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<130> 323-100USD

<140> 10/677,956

<141> 2003-10-01

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<150> 08/563,733

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<151> 1994-07-08

<150> 07/616,369

<151> 1990-11-21

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<151> 1990-08-27

<160> 76

<170> PatentIn version 3.3

<210> 1

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<221> CDS

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cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99
His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
15 20 25

gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147
Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
30 35 40

tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195
Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
45 50 55 60

ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243
Page 1

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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205